IN THE SPECIFICATION:

Please enter the substitute Specification included in the instant filing.

IN THE CLAIMS:

Please enter the following amended claims:

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1. (Currently amended) A method for identifying a ~~the~~ candidate protein ~~proteins~~ that may be useful as an anti-infective ~~infectives~~, which comprises:

i) calculating computationally ~~the~~ different sequence-based attributes from all ~~the~~ protein sequences of a ~~the~~ selected pathogenic organism, ~~organisms.~~

ii) clustering computationally all the protein sequences ~~the proteins~~ of said selected pathogenic organism ~~a genome~~ based on the ~~these~~ sequence-based attributes of step i) using Principle Component Analysis,

iii) identifying computationally ~~the~~ outlier protein ~~proteins~~ sequences from the selected pathogenic organism protein sequences which are excluded from a ~~the~~ main cluster,

iv) matching an ~~the~~ outlier protein sequence with ~~the~~ protein sequences in various databases,

v) selecting an ~~the~~ unique outlier protein sequence ~~sequences~~ not homologous to any ~~of the~~ protein sequence in said various databases ~~sequences~~ searched above, and

vi) validating computationally the protein sequence of step v) ~~sequences~~ as a candidate anti-infective ~~infectives~~ by comparing said sequence with ~~the~~ known protein sequences of the selected pathogenic organism that are biochemically characterized ~~in the pathogen.genome~~.

2. (Currently amended) The~~A~~ method according to ~~claimed in~~ claim 1, wherein~~,~~ the selected pathogenic organism is a member selected from the group consisting of *Borrelia burgdorferi, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Haemophilus influenzae, Helicobacter pylori, Leishmania major, Mycoplasma genetalium, Mycoplasma pneumoniae, Mycobacterium tuberculosis, Neisseria meningitis, Pseudomonas aeruginosa, Plasmodium falciparum, Rickettsia prowazekii, Treponema pallidum,* and *Vibrio cholerae*.~~protein sequence data is taken from any organism, specifically but not limited to organisms such as B.burgdorfei, C jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genetalium, M.pneumoniae, M.tuberculosis, N.meningitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, V.cholerae.~~

3. (Currently amended) The~~A~~ method according to ~~claimed in~~ claim 1, wherein said ~~different~~ sequence-based attributes are one or more of ~~used for identification of candidate anti-infective proteins are selected from the group co9mprising of~~ a fixed protein attribute, ~~and~~ one or more of a variable protein attribute~~attributes~~, or a combination thereof.

4. (Currently amended) The~~A~~ method according to ~~claimed in~~ claim 1, wherein said one or more ~~the~~ fixed protein attribute is ~~attributes are~~ selected from the group consisting ~~comprising~~ of percentage of charged amino acids, percentage hydrophobicity, distance of protein sequence from a fixed reference frame, measure of dipeptide complexity of said candidate protein, and measure of hydrophobic distance from a fixed reference frame.

5. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 3, wherein said one or more ~~the~~ variable protein attribute is ~~the~~ distance of said candidate ~~the protein~~ sequence from a variable reference frame.

6. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 1, wherein the clustering of step ii) ~~cluster analysis~~ is carried out by Principle Analysis Technique using correlation coefficient between the attributes.

7. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 1, wherein the steps i) ~~I~~ to iv) and vi) are performed computationally.

8. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 1, wherein the clustering of step ii) ~~the proteins~~ is based upon analysis of sequence attributes, and not upon ~~instead of~~ sequence pattern linked to biochemical functions. an unique outlier protein sequence not homologous to any protein sequence in said various databases

9. (Currently amended) The method according to ~~A methos as claimed in~~ claim 1, wherein the unique outlier protein sequence of step v) is a protein of one member selected from the group consisting of ~~sequences non-homologous to the known anti-infective sequences specifically in the following pathogens but not limited to, such as~~ *Borrelia burgdorferi, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Haemophilus influenzae, Helicobacter pylori, Leishmania major, Mycoplasma genetalium, Mycoplasma pneumoniae, Mycobacterium tuberculosis, Neisseria meningitis, Pseudomonas aeruginosa, Plasmodium falciparum, Rickettsia prowazekii, Treponema pallidum,* and *Vibrio cholerae*~~B.burgdorfei, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genetalium, M.pneumoniae, M.tuberculosis, N.meningitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, V.cholerae~~.

10. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 1~~-~~, wherein the unique outlier protein is a member selected from the group consisting of the amino acid sequences of

SEQ ID NOs:1-31.~~sequences obtained by the method of invention that can serve as potential anti-infective candidates as listed in Table 1 and list 1.~~

11. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 1-, wherein the ~~The~~ unique outlier protein is a member selected from the group consisting of the amino acid sequences of SEQ ID NOs:32-118~~hypothetical protein sequences from pathogenic genomes that can serve as anti-infective candidates listed in Table 2~~.

12. (Canceled).

13. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 1-, wherein all of said steps taking place computationally are performed on a ~~the~~ computer system comprising~~comprises~~:

a) ____a central processing unit (CPU) that (1) executes ~~, executing~~ DISTANCE program, (2) that executes a program that clusters ~~, clustering of the~~ protein sequences based on different attributes ~~using~~ by Principle Component Analysis, and (3) that stores all results ~~all stored~~ in a memory device accessed by said CPU-,

b) ____a display on which the CPU ~~central processing unit~~ displays all results ~~the screens~~ of ~~the above mentioned~~ said programs in response to user inputs; and

c) ____a user interface device.

14. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 1-, wherein the candidate ~~unique outlier hypothetical~~ protein may ~~sequences from pathogenic genomes that can~~ be used for a diagnostic purpose.

15. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 1-, wherein the candidate ~~unique outlier hypothetical~~ protein may ~~sequences from pathogenic genomes that can~~ be used as a vaccine candidate~~candidates~~.

16. (Currently amended) The~~A~~ method according to ~~as claimed in~~ claim 1~~-~~, wherein the candidate ~~The unique outlier hypothetical~~ protein may ~~sequences from pathogenic genomes that can~~ be used for a therapeutic purpose~~purposes~~.

17-19. (canceled).

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